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RAW SEQUENCE LISTING

DATE: 08/21/2002

PATENT APPLICATION: US/09/716,928A

TIME: 15:14:25

Input Set : A:\GI-20.txt

Output Set: N:\CRF4\08212002\I716928A.raw

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3 <110> APPLICANT: Dunussi-Joannopoulos, Kyriaki
5 <120> TITLE OF INVENTION: USE OF COMBINATION THERAPY COMPRISING A STIMULATORY
6   FORM OF A COSTIMULATORY MOLECULE AND A CHEMOTHERAPEUTIC
7   AGENT
9 <130> FILE REFERENCE: GNN-020
C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/716,928A
12 <141> CURRENT FILING DATE: 2000-11-20
14 <150> PRIOR APPLICATION NUMBER: USSN 60/247,329
15 <151> PRIOR FILING DATE: 2000-11-10
17 <160> NUMBER OF SEQ ID NOS: 12
19 <170> SOFTWARE: PatentIn Ver. 2.0
21 <210> SEQ ID NO: 1
22 <211> LENGTH: 1491
23 <212> TYPE: DNA
24 <213> ORGANISM: Homo sapiens
26 <220> FEATURE:
27 <221> NAME/KEY: CDS
28 <222> LOCATION: (318)..(1181)
30 <220> FEATURE:
31 <221> NAME/KEY: mat_peptide
32 <222> LOCATION: (420)
34 <220> FEATURE:
35 <223> OTHER INFORMATION: Open reading frame from location 318 to 1181 bp
37 <220> FEATURE:
38 <223> OTHER INFORMATION: Alternate polyadenylation signal from location
39   1474 to 1479 bp
41 <400> SEQUENCE: 1
42 ccaaagaaaa agtgatttgt cattgcttta tagactgtaa gaagagaaca tctcagaagt 60
44 ggagtcttac cctgaaatca aaggatttaa agaaaaagtg gaatttttct tcagcaagct 120
46 gtgaaactaa atccacaacc ttggagacc caggaacacc ctccaatctc tgtgtgtttt 180
48 gtaaacaatca ctggagggtc ttctacgtga gcaattggat tgatcatcagc cctgcctgtt 240
50 ttgcacctgg gaagtgcctt ggtcttactt gggtcctaat tgttggtttt cacttttgac 300
52 cctaagcatc tgaagcc atg ggc cac aca cgg agg cag gga aca tca cca 350
53           Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro
54           -30                      -25
56 tcc aag tgt cca tac ctg aat ttc ttt cag ctg ttg gtg ctg gct ggt 398
57 Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly
58           -20                      -15                      -10
60 ctt tct cac ttc tgt tca ggt gtt atc cac gtg acc aag gaa gtg aaa 446
61 Leu Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys
62           -5                      -1    1                      5
64 gaa gtg gca acg ctg tcc tgt ggt cac aat gtt tct gtt gaa gag ctg 494
65 Glu Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu

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66 10          15          20          25
68 gca caa act cgc atc tac tgg caa aag gag aag aaa atg gtg ctg act 542
69 Ala Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr
70          30          35          40
72 atg atg tct ggg gac atg aat ata tgg ccc gag tac aag aac cgg acc 590
73 Met Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr
74          45          50          55
76 atc ttt gat atc act aat aac ctc tcc att gtg atc ctg gct ctg cgc 638
77 Ile Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg
78          60          65          70
80 cca tct gac gag ggc aca tac gag tgt gtt gtt ctg aag tat gaa aaa 686
81 Pro Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys
82          75          80          85
84 gac gct ttc aag cgg gaa cac ctg gct gaa gtg acg tta tca gtc aaa 734
85 Asp Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys
86 90          95          100          105
88 gct gac ttc cct aca cct agt ata tct gac ttt gaa att cca act tct 782
89 Ala Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser
90          110          115          120
92 aat att aga agg ata att tgc tca acc tct gga ggt ttt cca gag cct 830
93 Asn Ile Arg Arg Ile Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro
94          125          130          135
96 cac ctc tcc tgg ttg gaa aat gga gaa gaa tta aat gcc atc aac aca 878
97 His Leu Ser Trp Leu Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr
98          140          145          150
100 aca gtt tcc caa gat cct gaa act gag ctc tat gct gtt agc agc aaa 926
101 Thr Val Ser Gln Asp Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys
102          155          160          165
104 ctg gat ttc aat atg aca acc aac cac agc ttc atg tgt ctc atc aag 974
105 Leu Asp Phe Asn Met Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys
106 170          175          180          185
108 tat gga cat tta aga gtg aat cag acc ttc aac tgg aat aca acc aag 1022
109 Tyr Gly His Leu Arg Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys
110          190          195          200
112 caa gag cat ttt cct gat aac ctg ctc cca tcc tgg gcc att acc tta 1070
113 Gln Glu His Phe Pro Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu
114          205          210          215
116 atc tca gta aat gga att ttt gtg ata tgc tgc ctg acc tac tgc ttt 1118
117 Ile Ser Val Asn Gly Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe
118          220          225          230
120 gcc cca aga tgc aga gag aga agg agg aat gag aga ttg aga agg gaa 1166
121 Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu
122          235          240          245
124 agt gta cgc cct gta taacagtgtc cgcagaagca aggggctgaa aagatctgaa 1221
125 Ser Val Arg Pro Val
126 250
128 ggtagcctcc gtcattctctt ctgggataca tggatcgtgg ggatcatgag gcattcttcc 1281
130 cttaacaaat ttaagctgtt ttaccacta cctcaccttc ttaaaaacct ctttcagatt 1341
132 aagctgaaca gttacaagat ggctggcatt cctctccttt ctccccatat gcaatttgct 1401

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134 taatgtaacc tcttcttttg ccatgtttcc attctgccat cttgaattgt cttgtcagcc 1461
136 aattcattat ctattaaaca ctaatttgag 1491
139 <210> SEQ ID NO: 2
140 <211> LENGTH: 288
141 <212> TYPE: PRT
142 <213> ORGANISM: Homo sapiens
144 <400> SEQUENCE: 2
145 Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr
146 -30 -25 -20
148 Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys
149 -15 -10 -5
151 Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu Val Ala Thr Leu
152 -1 1 5 10
154 Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala Gln Thr Arg Ile
155 15 20 25 30
157 Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met Met Ser Gly Asp
158 35 40 45
160 Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile Phe Asp Ile Thr
161 50 55 60
163 Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro Ser Asp Glu Gly
164 65 70 75
166 Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp Ala Phe Lys Arg
167 80 85 90
169 Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala Asp Phe Pro Thr
170 95 100 105 110
172 Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn Ile Arg Arg Ile
173 115 120 125
175 Ile Cys Ser Thr Ser Gly Gly Phe Pro Glu Pro His Leu Ser Trp Leu
176 130 135 140
178 Glu Asn Gly Glu Glu Leu Asn Ala Ile Asn Thr Thr Val Ser Gln Asp
179 145 150 155
181 Pro Glu Thr Glu Leu Tyr Ala Val Ser Ser Lys Leu Asp Phe Asn Met
182 160 165 170
184 Thr Thr Asn His Ser Phe Met Cys Leu Ile Lys Tyr Gly His Leu Arg
185 175 180 185 190
187 Val Asn Gln Thr Phe Asn Trp Asn Thr Thr Lys Gln Glu His Phe Pro
188 195 200 205
190 Asp Asn Leu Leu Pro Ser Trp Ala Ile Thr Leu Ile Ser Val Asn Gly
191 210 215 220
193 Ile Phe Val Ile Cys Cys Leu Thr Tyr Cys Phe Ala Pro Arg Cys Arg
194 225 230 235
196 Glu Arg Arg Arg Asn Glu Arg Leu Arg Arg Glu Ser Val Arg Pro Val
197 240 245 250
200 <210> SEQ ID NO: 3
201 <211> LENGTH: 1120
202 <212> TYPE: DNA
203 <213> ORGANISM: Homo sapiens
205 <220> FEATURE:
206 <221> NAME/KEY: CDS

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207 <222> LOCATION: (107)..(1093)

209 <400> SEQUENCE: 3

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210 cacaggggtga aagcttttgc tctctgctgc tgtaacaggg actagcacag acacaaggat 60
212 gagtgggggtc atttccagat attaggtcac agcagaagca gccaaa atg gat ccc 115
213                                     Met Asp Pro
214                                     1
216 cag tgc act atg gga ctg agt aac att ctc ttt gtg atg gcc ttc ctg 163
217 Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu
218      5                      10                      15
220 ctc tct ggt gct gct cct ctg aag att caa gct tat ttc aat gag act 211
221 Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr
222 20                      25                      30                      35
224 gca gac ctg cca tgc caa ttt gca aac tct caa aac caa agc ctg agt 259
225 Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser
226      40                      45                      50
228 gag cta gta gta ttt tgg cag gac cag gaa aac ttg gtt ctg aat gag 307
229 Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu
230      55                      60                      65
232 gta tac tta ggc aaa gag aaa ttt gac agt gtt cat tcc aag tat atg 355
233 Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met
234      70                      75                      80
236 ggc cgc aca agt ttt gat tcg gac agt tgg acc ctg aga ctt cac aat 403
237 Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn
238      85                      90                      95
240 ctt cag atc aag gac aag ggc ttg tat caa tgt atc atc cat cac aaa 451
241 Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys
242 100                      105                      110                      115
244 aag ccc aca gga atg att cgc atc cac cag atg aat tct gaa ctg tca 499
245 Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser
246      120                      125                      130
248 gtg ctt gct aac ttc agt caa cct gaa ata gta cca att tct aat ata 547
249 Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile
250      135                      140                      145
252 aca gaa aat gtg tac ata aat ttg acc tgc tca tct ata cac ggt tac 595
253 Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr
254      150                      155                      160
256 cca gaa cct aag aag atg agt gtt ttg cta aga acc aag aat tca act 643
257 Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr
258      165                      170                      175
260 atc gag tat gat ggt att atg cag aaa tct caa gat aat gtc aca gaa 691
261 Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu
262 180                      185                      190                      195
264 ctg tac gac gtt tcc atc agc ttg tct gtt tca ttc cct gat gtt acg 739
265 Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr
266      200                      205                      210
268 agc aat atg acc atc ttc tgt att ctg gaa act gac aag acg cgg ctt 787
269 Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu
270      215                      220                      225
272 tta tct tca cct ttc tct ata gag ctt gag gac cct cag cct ccc cca 835

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273 Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro
274      230      235      240
276 gac cac att cct tgg att aca gct gta ctt cca aca gtt att ata tgt 883
277 Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys
278      245      250      255
280 gtg atg gtt ttc tgt cta att cta tgg aaa tgg aag aag aag cgg 931
281 Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Arg
282 260      265      270      275
284 cct cgc aac tct tat aaa tgt gga acc aac aca atg gag agg gaa gag 979
285 Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu
286      280      285      290
288 agt gaa cag acc aag aaa aga gaa aaa atc cat ata cct gaa aga tct 1027
289 Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser
290      295      300      305
292 gat gaa gcc cag cgt gtt ttt aaa agt tcg aag aca tct tca tgc gac 1075
293 Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp
294      310      315      320
296 aaa agt gat aca tgt ttt taattaaaga gtaaagccca aaaaaaa 1120
297 Lys Ser Asp Thr Cys Phe
298      325
301 <210> SEQ ID NO: 4
302 <211> LENGTH: 329
303 <212> TYPE: PRT
304 <213> ORGANISM: Homo sapiens
306 <400> SEQUENCE: 4
307 Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
308 1      5      10      15
310 Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
311      20      25      30
313 Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
314      35      40      45
316 Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
317 50      55      60
319 Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
320 65      70      75      80
322 Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
323      85      90      95
325 Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
326      100      105      110
328 His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
329      115      120      125
331 Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
332      130      135      140
334 Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
335 145      150      155      160
337 His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
338      165      170      175
340 Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
341      180      185      190

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VERIFICATION SUMMARY

PATENT APPLICATION: US/09/716,928A

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number